

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/758,498DATE: 03/22/2001
TIME: 22:54:18

INPUT SET: S36549.raw

OIIPE 0400
03/07/01

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

ENTERED

1
2
3 (1) General Information
4
5 (i) APPLICANT: Lal, Preeti
6 Corley, Neil C.
7 Tang, Y. Tom
8
9 (ii) TITLE OF THE INVENTION: AUTOANTIGEN-LIKE PROTEIN
10
11
12 (iii) NUMBER OF SEQUENCES: 3
13
14 (iv) CORRESPONDENCE ADDRESS:
15 (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
16 (B) STREET: 3174 Porter Drive
17 (C) CITY: Palo Alto
18 (D) STATE: CA
19 (E) COUNTRY: USA
20 (F) ZIP: 94304
21
22 (v) COMPUTER READABLE FORM:
23 (A) MEDIUM TYPE: Diskette
24 (B) COMPUTER: IBM Compatible
25 (C) OPERATING SYSTEM: DOS
26 (D) SOFTWARE: FastSEQ for Windows Version 2.0
27
28 (vi) CURRENT APPLICATION DATA:
29 (A) APPLICATION NUMBER: 09/758,498
30 (B) FILING DATE:
31 (C) CLASSIFICATION:
32
33 (vii) PRIOR APPLICATION DATA:
34 (A) APPLICATION NUMBER: 08/928,442
35 (B) FILING DATE:
36
37 (viii) ATTORNEY/AGENT INFORMATION:
38 (A) NAME: Billings, Lucy J.
39 (B) REGISTRATION NUMBER: 36,749
40 (C) REFERENCE/DOCKET NUMBER: PF-0385 US
41
42 (ix) TELECOMMUNICATION INFORMATION:
43 (A) TELEPHONE: 650-855-0555
44 (B) TELEFAX: 650-845-4166
45 (C) TELEX:
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RAW SEQUENCE LISTING PATENT APPLICATION US/09/758,498

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 395 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: HUVENOB01

(B) CLONE: 35842

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met	Phe	Pro	Arg	Val	Ser	Thr	Phe	Leu	Pro	Leu	Arg	Pro	Leu	Ser	Arg
1				5				10					15		
His	Pro	Leu	Ser	Ser	Gly	Ser	Pro	Glu	Thr	Ser	Ala	Ala	Ala	Ile	Met
			20					25					30		
Leu	Leu	Thr	Val	Arg	His	Gly	Thr	Val	Arg	Tyr	Arg	Ser	Ser	Ala	Leu
		35					40					45			
Leu	Ala	Arg	Thr	Lys	Asn	Asn	Ile	Gln	Arg	Tyr	Phe	Gly	Thr	Asn	Ser
	50					55				60					
Val	Ile	Cys	Ser	Lys	Lys	Asp	Lys	Gln	Ser	Val	Arg	Thr	Glu	Glu	Thr
	65				70					75				80	
Ser	Lys	Glu	Thr	Ser	Glu	Ser	Gln	Asp	Ser	Glu	Lys	Glu	Asn	Thr	Lys
				85				90					95		
Lys	Asp	Leu	Leu	Gly	Ile	Ile	Lys	Gly	Met	Lys	Val	Glu	Leu	Ser	Thr
			100					105					110		
Val	Asn	Val	Arg	Thr	Thr	Lys	Pro	Pro	Lys	Arg	Arg	Pro	Leu	Lys	Ser
		115					120					125			
Leu	Glu	Ala	Thr	Leu	Gly	Arg	Leu	Arg	Arg	Ala	Thr	Glu	Tyr	Ala	Pro
	130					135					140				
Lys	Lys	Arg	Ile	Glu	Pro	Leu	Ser	Pro	Glu	Leu	Val	Ala	Ala	Ala	Ser
	145					150				155				160	
Ala	Val	Ala	Asp	Ser	Leu	Pro	Phe	Asp	Lys	Gln	Thr	Thr	Lys	Ser	Glu
			165					170					175		
Leu	Leu	Ser	Gln	Leu	Gln	Gln	His	Glu	Glu	Glu	Ser	Arg	Ala	Gln	Arg
			180					185					190		
Asp	Ala	Lys	Arg	Pro	Lys	Ile	Ser	Phe	Ser	Asn	Ile	Ile	Ser	Asp	Met
		195					200					205			
Lys	Val	Ala	Arg	Ser	Ala	Thr	Ala	Arg	Val	Arg	Ser	Arg	Pro	Glu	Leu
	210					215					220				
Arg	Ile	Gln	Phe	Asp	Glu	Gly	Tyr	Asp	Asn	Tyr	Pro	Gly	Gln	Glu	Lys
	225					230				235				240	
Thr	Asp	Asp	Leu	Lys	Lys	Arg	Lys	Asn	Ile	Phe	Thr	Gly	Lys	Arg	Leu
			245					250					255		
Asn	Ile	Phe	Asp	Met	Met	Ala	Val	Thr	Lys	Glu	Ala	Pro	Glu	Thr	Asp
			260					265					270		
Thr	Ser	Pro	Ser	Leu	Trp	Asp	Val	Glu	Phe	Ala	Lys	Gln	Leu	Ala	Thr
		275					280					285			
Val	Asn	Glu	Gln	Pro	Leu	Gln	Asn	Gly	Phe	Glu	Glu	Leu	Ile	Gln	Trp
	290					295						300			

RAW SEQUENCE LISTING PATENT APPLICATION US/09/758,498

DATE: 03/22/2001
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100  Thr Lys Glu Gly Lys Leu Trp Glu Phe Pro Ile Asn Asn Glu Ala Gly
101  305                               310 315                               320
102  Phe Asp Asp Asp Gly Ser Glu Phe His Glu His Ile Phe Leu Glu Lys
103  325                               330                               335
104  His Leu Glu Ser Phe Pro Lys Gln Gly Pro Ile Arg His Phe Met Glu
105  340                               345                               350
106  Leu Val Thr Cys Gly Leu Ser Lys Asn Pro Tyr Leu Ser Val Lys Gln
107  355                               360                               365
108  Lys Val Glu His Ile Glu Trp Phe Arg Asn Tyr Phe Asn Glu Lys Lys
109  370                               375                               380
110  Asp Ile Leu Lys Glu Ser Asn Ile Gln Phe Asn
111  385                               390                               395

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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1314 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: HUVENOB01
- (B) CLONE: 35842

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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127  GACGTGTTTG GCAGCGGGAC GCACCATTTC AGTTGTGTTC TTGGTTCATT TCGTGCTCG      60
128  GCGATGTTTC CTAGAGTCTC GACGTTTCCTA CCTCTTCGCC CCCTTTCCCG CCACCCTTTG      120
129  TCCTCTGGAA GCCCGGAGAC ATCAGCGGCT GCGATTATGC TACTCACTGT TCGGCACGGA      180
130  ACAGTCAGGT ACCGCAGTTC AGCGCTGTTG GCCCGGACAA AAAATAACAT CCAAAGATAT      240
131  TTTGGCACTA ACAGTGTGAT CTGTAGCAAG AAAGATAAGC AGTCTGTTCG AACTGAGGAG      300
132  ACTTCCAAGG AGACTTCAGA GAGCCAAGAC AGTGAAAAGG AAAATACGAA AAAAGACTTG      360
133  TTAGGCATTA TTAAGGGCAT GAAAGTTGAA TTAAGCACAG TAAATGTACG AACAACAAAG      420
134  CCCCCCAAAA GAAGACCACT TAAAAGTTTG GAAGCTACAC TTGGCAGGCT TCGAAGAGCT      480
135  ACAGAATATG CTCCAAAGAA GAGAATTGAG CCCCTGAGTC CTGAGTTGGT GGCAGCTGCA      540
136  TCTGCTGTGG CAGATTCTCT CCCTTTTGAT AAGCAAACAA CCAAGTCAGA GCTGCTGAGC      600
137  CAGCTCCAGC AGCATGAGGA AGAGTCAAGG GCACAGAGAG ATGCAAAGCG ACCTAAAATT      660
138  AGTTTCAGTA ACATAATATC AGATATGAAA GTTGCCAGAT CTGCTACAGC TAGAGTTCGT      720
139  TCAAGACCAG AGCTTCGGAT TCAGTTTGAT GAAGGCTATG ACAATTATCC TGGCCAGGAG      780
140  AAGACGGATG ATCTTAAAAA AAGGAAAAAT ATATTCACAG GGAAAAGACT TAATATTTT      840
141  GACATGATGG CAGTTACTAA AGAAGCACCT GAAACAGACA CATCACCTTC ACTTTGGGAT      900
142  GTGGAATTTG CTAAGCAGTT AGCCACAGTA AATGAACAAC CCCTTCAGAA TGGATTTGAA      960
143  GAGCTGATCC AGTGGACAAA AGAGGGGAAA CTATGGGAGT TCCCAATTAA CAATGAAGCA      1020
144  GGTTTTGATG ATGATGGTTC AGAATTTTCAT GAACATATAT TTCTGGAGAA ACACCTGGAG      1080
145  AGCTTTCCAA AACAAGGACC AATTCGCCAC TTCATGGAGC TGGTGACTTG TGGCCTTTCC      1140
146  AAAAACCCAT ATCTTAGTGT TAAACAGAAG GTTGAACACA TAGAGTGGTT TAGAAATTAT      1200
147  TTTAATGAAA AAAAGGATAT TCTAAAAGAA AGTAACATAC AGTTCAATTA AGACCATGGA      1260
148  AATTTTATT TCAAACAATT AGAGATGGAT ATTACAATAA AATAAAATAA TTGC          1314

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(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

RAW SEQUENCE LISTING PATENT APPLICATION US/09/758,498

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TIME: 22:54:19

INPUT SET: S36549.raw

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153         (A) LENGTH: 384 amino acids
154         (B) TYPE: amino acid
155         (C) STRANDEDNESS: single
156         (D) TOPOLOGY: linear
157
158     (vii) IMMEDIATE SOURCE:
159         (A) LIBRARY: GenBank
160         (B) CLONE: 1272669
161
162     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
163
164     Met Leu His Arg Ile Pro Ala Phe Leu Arg Pro Arg Pro Phe Ser Gly
165         1             5             10             15
166     Leu Pro Leu Ser Cys Gly Asn Arg Asp Val Ser Val Ala Val Leu Pro
167         20             25             30
168     Ala Ala Gln Ser Gly Ala Val Arg Thr Glu Asn Asn Ile Gln Arg His
169         35             40             45
170     Phe Cys Thr Ser Arg Ser Ile Cys Ser Lys Lys Val Asp Gln Ser Val
171         50             55             60
172     Pro Ala Asn Glu Ile Ser Gln Lys Ala Ala Glu Ser Gln Gly Arg Gly
173         65             70             75             80
174     Lys Glu Thr Leu Lys Lys Asp Leu Leu Asp Ile Ile Lys Asp Met Lys
175         85             90             95
176     Val Asp Leu Ser Thr Ala Asn Val Lys Thr Pro Lys Pro Arg Gly Arg
177         100            105            110
178     Lys Pro Ser Ala Ser Leu Glu Ala Thr Val Asp Arg Leu Gln Lys Ala
179         115            120            125
180     Pro Glu Asp Pro Pro Lys Lys Arg Asn Glu Phe Leu Ser Pro Glu Leu
181         130            135            140
182     Val Ala Ala Ala Ser Ala Val Ala Asp Ser Leu Pro Phe Asp Lys Gln
183         145            150            155            160
184     Thr Thr Lys Ser Glu Leu Leu Arg Gln Leu Gln Gln His Glu Glu Glu
185         165            170            175
186     Leu Arg Ala Gln Lys Asp Arg Glu Lys Arg Arg Ile Ser Phe Thr His
187         180            185            190
188     Ile Ile Ser Asn Met Lys Ile Ala Lys Ser Pro Ser Gly Arg Ala Ser
189         195            200            205
190     Thr Arg Pro Gln His Gln Ile Gln Phe Asp Glu Asp Met Asp Ser Ser
191         210            215            220
192     Leu Lys Gln Glu Lys Pro Thr Asp Phe Arg Lys Arg Lys Tyr Leu Phe
193         225            230            235            240
194     Lys Gly Lys Arg Leu Ser Ile Phe Ala Asp Lys Ala Phe Ala Asp Glu
195         245            250            255
196     Pro Pro Glu Pro Glu Ala Ser Pro Ser Leu Trp Glu Ile Glu Phe Ala
197         260            265            270
198     Lys Gln Leu Ala Ser Val Ala Asp Gln Pro Phe Glu Asn Gly Phe Glu
199         275            280            285
200     Glu Met Ile Gln Trp Thr Lys Glu Gly Lys Leu Trp Glu Phe Pro Val
201         290            295            300
202     Asn Asn Glu Ala Gly Leu Asp Asp Asp Gly Ser Glu Phe His Glu His
203         305            310            315            320
204     Ile Phe Leu Asp Lys Tyr Leu Glu Asp Phe Pro Lys Gln Gly Pro Ile
205         325            330            335

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RAW SEQUENCE LISTING
PATENT APPLICATION *US/09/758,498*

INPUT SET: S36549.raw

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PAGE: 1

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/09/758,498

DATE: 03/22/2001
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Original Text